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Query= SEQ ID NO:1
(3963 letters)

Sequences producing significant alignments:

Score E
(bits) Value

AC024258.9.1.160658
AL512429.14.1.11170
AC016395.5.1.166869

1794 0.0
1159 0.0
442 e-121

>AC024258.9.1.160658
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Identities = 904/904 (100%)
Strand = Plus / Plus

Query: 1 atgcaagacgacagcatagaagcttctacttccatatctcagcttctaagagagagctat 60
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Sbjct: 110106 atgcaagacgacagcatagaagcttctacttccatatctcagcttctaagagagagctat 110165

Query: 61 ttagctgaaaccagacatcggggaaacaatgagaggagtcgagcggagccctcctccaac 120
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Query: 301 tctcctgatcagatgaaacactcacctaatttaagttttgagcctaacttctgccaggat 360
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Query: 421 tgttctgaaacccagtcacaaaaaagtatttttaataaggctgccgacttcattgaagag 480
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Query: 481 ctatcctcccttttcaaattccacagctccaaaaggattagacctcgtgcctgcaaaaac 540
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Query: 661 gataatgaagtgaatcacgccctggaacagcaggaagccaagaggcgtgaagcggagcag 720
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Query: 901 aggt 904
 |||
 Sbjct: 111006 aggt 111009

Score = 728 bits (367), Expect = 0.0
 Identities = 372/375 (99%)
 Strand = Plus / Plus

Query: 1599 aggaaatgaggacctcagcaacaacgggtctcttcactcagccaactcyaccaccaacct 1658
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 Sbjct: 154959 aggaaatgaggacctcagcaacaacgggtctcttcactcagccaactctaccaccaacct 155018

Query: 1659 ggcagctattgagccacagccctccccacccactcagagcctccatctgtggaacaacc 1718
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 Sbjct: 155019 ggcagctattgagccacagccctccccacccactcagagcctccatctgtggaacaacc 155078

Query: 1719 ccccaaaccctcgagggggttctggtgaaccacaatgagccccgggtccagctccag 1778
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 Sbjct: 155079 ccccaaaccctcgagggggttctggtgaaccacaatgagccccgggtccagctccag 155138

Query: 1779 gattgggcttcgtgtgcacttcaacctgcctgaagatgacaaaggaagtgaagcatcctc 1838
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 Sbjct: 155139 gattgggcttcgtgtgcacttcaacctgcctgaagatgacaaaggaagtgaagcatcctc 155198

Query: 1839 cgaggctggtgtggtgaccaccagacagaccaggcccgattctttscaggagaggttcaa 1898
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Sbjct: 155199 cgaggctggtgtggtgaccaccagacagaccaggcccgattctttccaggagaggttcaa 155258

Query: 1899 cggacaggcaacaaaaacccagagccttctttccccgtgaaagagccccctccagttct 1958
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Sbjct: 155259 cggacaggcaacaaaaacccagagccttctttccccgtgaaagagccccctccagttct 155318

Query: 1959 ggccaaaccctaaact 1973
 ||||||||||||||||
 Sbjct: 155319 ggccaaaccctaaact 155333

Score = 355 bits (179), Expect = 1e-94
 Identities = 179/179 (100%)
 Strand = Plus / Plus

Query: 901 aggtggtactgtgaaggcaaggagcttgaaaattccccagatattcacatcggtccaggca 960
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Sbjct: 131605 aggtggtactgtgaaggcaaggagcttgaaaattccccagatattcacatcggtccaggca 131664

Query: 961 ggaaatctgcactcactgaccattgcggaagcctttgaagaggacacaggacgctattcc 1020
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Sbjct: 131665 ggaaatctgcactcactgaccattgcggaagcctttgaagaggacacaggacgctattcc 131724

Query: 1021 tgctttgcttctaacaatctatgggacagattcgacttctgctgagatttatatagaagg 1079
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Sbjct: 131725 tgctttgcttctaacaatctatgggacagattcgacttctgctgagatttatatagaagg 131783

Score = 286 bits (144), Expect = 9e-74
 Identities = 144/144 (100%)
 Strand = Plus / Plus

Query: 1316 agatgctacaaaatttgtcagcttctgagggtcagctgggtgtctttgaatgcagagtaa 1375
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Sbjct: 147151 agatgctacaaaatttgtcagcttctgagggtcagctgggtgtctttgaatgcagagtaa 147210

Query: 1376 aaggagctccatctcctaagggttgagtggatatagagaagggactttaatagaagattctc 1435
|||||
Sbjct: 147211 aaggagctccatctcctaagggttgagtggatatagagaagggactttaatagaagattctc 147270

Query: 1436 cagatttttaggattttacagaaaa 1459
|||||
Sbjct: 147271 cagatttttaggattttacagaaaa 147294

Score = 238 bits (120), Expect = 2e-59
Identities = 120/120 (100%)
Strand = Plus / Plus

Query: 1482 agaggagatttgcaccttggtcattgctgaggtggttgcagaagattctgggtgcttcac 1541
|||||
Sbjct: 154367 agaggagatttgcaccttggtcattgctgaggtggttgcagaagattctgggtgcttcac 154426

Query: 1542 atgtactgcaagcaacaaatacggcacagtgtcaagcattgcacagctgcacgtgagagg 1601
|||||
Sbjct: 154427 atgtactgcaagcaacaaatacggcacagtgtcaagcattgcacagctgcacgtgagagg 154486

Score = 230 bits (116), Expect = 5e-57
Identities = 116/116 (100%)
Strand = Plus / Plus

Query: 1130 gaatccagaagccaaatgaggtgtcatctcctcccactacctctgcagtcattcctccag 1189
|||||
Sbjct: 137019 gaatccagaagccaaatgaggtgtcatctcctcccactacctctgcagtcattcctccag 137078

Query: 1190 cagtaccccaagcccagcatttggtggcccaacctcggtgtggcaaccatccagcag 1245
|||||
Sbjct: 137079 cagtaccccaagcccagcatttggtggcccaacctcggtgtggcaaccatccagcag 137134

Score = 149 bits (75), Expect = 1e-32
Identities = 75/75 (100%)
Strand = Plus / Plus

Query: 1243 cagtgtcagagccccaccaattacttgcagggattggatggaaaacctatcattgcagct 1302
|||||
Sbjct: 138704 cagtgtcagagccccaccaattacttgcagggattggatggaaaacctatcattgcagct 138763

Query: 1303 cctgtgtttacaaag 1317
|||||
Sbjct: 138764 cctgtgtttacaaag 138778

Score = 107 bits (54), Expect = 5e-20
Identities = 54/54 (100%)
Strand = Plus / Plus

Query: 1077 aggggtttcttcttctgactcagaaggcgaccctaacaaggaagagatgaatcg 1130
|||||
Sbjct: 134140 aggggtttcttcttctgactcagaaggcgaccctaacaaggaagagatgaatcg 134193

Score = 48.1 bits (24), Expect = 0.041
Identities = 24/24 (100%)
Strand = Plus / Plus

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Sbjct: 150396 aacctcgatccatggcagagccag 150419

>AL512429.14.1.11170
Length = 11170

Score = 1159 bits (584), Expect = 0.0
Identities = 588/592 (99%)
Strand = Plus / Plus

Query: 1974 tgattccactcagttacaacagcttcataaccaagtcttactggaacaacaccaattgca 2033
|||||
Sbjct: 4075 tgattccactcagttacaacagcttcataaccaagtcttactggaacaacaccaattgca 4134

Query: 2034 aaaccacctccttcattctcctaaggagtttcctttcarcatgactgttttgaactccaa 2093
|||||
Sbjct: 4135 aaaccacctccttcattctcctaaggagtttcctttcagcatgactgttttgaactccaa 4194

Query: 2094 tgctccccagcggtgacaacatccartaagcaggtgaaggctccttcattcacagacggt 2153
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Sbjct: 4195 tgctccccagcggtgacaacatccagtaagcaggtgaaggctccttcattcacagacggt 4254

Query: 2154 cagcttggtccggccgaagtattttcttccctccacgaacaccaccgcagcaactgtggc 2213
|||||
Sbjct: 4255 cagcttggtccggccgaagtattttcttccctccacgaacaccaccgcagcaactgtggc 4314

Query: 2214 cccttcagctctccggtgttcactttgagcagcactcctcaaactattcagaggacagt 2273
|||||
Sbjct: 4315 cccttcagctctccggtgttcactttgagcagcactcctcaaactattcagaggacagt 4374

Query: 2274 gagcaaagaaagcctcttagtggtctcaccctctgtgcaaaccaaatctccaggagggt 2333
|||||
Sbjct: 4375 gagcaaagaaagcctcttagtggtctcaccctctgtgcaaaccaaatctccaggagggt 4434

Query: 2334 ttccatccaaaatgagccactcccaccaggcccaacagaaccracaccaccattcac 2393
|||||
Sbjct: 4435 ttccatccaaaatgagccactcccaccaggcccaacagaaccaacaccaccattcac 4494

Query: 2394 attttccatccccagcggaaccagtttcagccccgctgtgtgtccccaattcctgtctc 2453
|||||
Sbjct: 4495 attttccatccccagcggaaccagtttcagccccgctgtgtgtccccaattcctgtctc 4554

Query: 2454 tcctaccagccggattcagaaccagtggtttctcagctctgttctgccttctctccc 2513
|||||
Sbjct: 4555 tcctaccagccggattcagaaccagtggtttctcagctctgttctgccttctctccc 4614

Query: 2514 tgccatcccacccacaaatgccatggrgctgcctagaagtgcaccatccatg 2565
|||||
Sbjct: 4615 tgccatcccacccacaaatgccatggggctgcctagaagtgcaccatccatg 4666

Score = 278 bits (140), Expect = 2e-71
Identities = 140/140 (100%)
Strand = Plus / Plus

Query: 2565 gccatcccagggttagcggaagaaaaatacaaagtctcctcaaccagtgaatgatgataa 2624
|||||
Sbjct: 5332 gccatcccagggttagcggaagaaaaatacaaagtctcctcaaccagtgaatgatgataa 5391

Query: 2625 cattcgtgaaactaagaacgcagtgattcgagacttggggaaaaaaataactttcagtga 2684
|||||
Sbjct: 5392 cattcgtgaaactaagaacgcagtgattcgagacttggggaaaaaaataactttcagtga 5451

Query: 2685 tgtcagaccaaaccagcagg 2704
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Sbjct: 5452 tgtcagaccaaaccagcagg 5471

>AC016395.5.1.166869

Length = 166869

Score = 442 bits (223), Expect = e-121

Identities = 226/227 (99%)

Strand = Plus / Minus

Query: 2701 caggagtacaaaatttcaagctttgagcagaggctgatgaatgaaatagagtttcgcttg 2760
|||||
Sbjct: 157129 caggagtacaaaatttcaagctttgagcagaggctgatgaatgaaatagagtttcgcttg 157070

Query: 2761 gaacgtactcctgttgatgaatcagatgatgaaattcaacatgatgagatccccacgggc 2820
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Sbjct: 157069 gaacgtactcctgttgatgaatcagatgatgaaattcaacatgatgagatccccacgggc 157010

Query: 2821 aagtgtattgctcccatctttgacaagagactcaagcacttccgggtcacagaaggctct 2880
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Sbjct: 157009 aagtgtattgctcccatctttgacaagagactcaagcacttccgggtcacagaaggctct 156950

Query: 2881 ccagtcacattcacctgcaaaaattggtgggatacctgttccaaaggt 2927
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Sbjct: 156949 ccagttacattcacctgcaaaaattggtgggatacctgttccaaaggt 156903

Score = 417 bits (210), Expect = e-113

Identities = 210/210 (100%)

Strand = Plus / Minus

Query: 3284 aggtgagtggtttaccgcccccgagctgacatggctactcaatggccaacctgtgctac 3343
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Query: 3344 cagatgcctcccacaagatgctggtcagggagaccggagtcactctctgctcattgacc 3403
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Sbjct: 146605 cagatgcctcccacaagatgctggtcagggagaccggagtcactctctgctcattgacc 146546

Query: 3404 cactcactcagcgcgacgcagggacctataagtgcacgctaccaaaaaaccgggcaga 3463
|||||
Sbjct: 146545 cactcactcagcgcgacgcagggacctataagtgcacgctaccaaaaaaccgggcaga 146486

Query: 3464 attcttttagtctggagctctctgtagtag 3493
|||||
Sbjct: 146485 attcttttagtctggagctctctgtagtag 146456

Score = 339 bits (171), Expect = 6e-90
Identities = 171/171 (100%)
Strand = Plus / Minus

Query: 3793 gctcagtggcaccatcagatcccaccgcccattgtctgtccggcccagtggcagtcgctac 3852
|||||
Sbjct: 135746 gctcagtggcaccatcagatcccaccgcccattgtctgtccggcccagtggcagtcgctac 135687

Query: 3853 ggatctctcaccagtaaaggacttgacatattttctgccttttctccatggaaagcacg 3912
|||||
Sbjct: 135686 ggatctctcaccagtaaaggacttgacatattttctgccttttctccatggaaagcacg 135627

Query: 3913 atgggtgattcatgctcttctcggagtgtagtggagagtgatgaacttta 3963
|||||
Sbjct: 135626 atgggtgattcatgctcttctcggagtgtagtggagagtgatgaacttta 135576

Score = 333 bits (168), Expect = 4e-88
Identities = 168/168 (100%)
Strand = Plus / Minus

Query: 3492 agccaaagaggtgaagaaagcacctgtgatcctggagaaactacagaactgcggtgttcc 3551
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Sbjct: 144204 agccaaagaggtgaagaaagcacctgtgatcctggagaaactacagaactgcggtgttcc 144145

Query: 3552 cgaaggccaccccgtgagactggagtgccgcgtgataggcatgccccacctgtgttcta 3611
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Sbjct: 144144 cgaaggccaccccgtgagactggagtgccgcgtgataggcatgccccacctgtgttcta 144085

Query: 3612 ctggaagaaagacaatgagaccatcccttgaccagagagaggatcag 3659
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Score = 306 bits (154), Expect = 9e-80
Identities = 158/159 (99%), Gaps = 1/159 (0%)
Strand = Plus / Minus

Query: 2924 aggtttactggttcaaagatgggaagcagatttctaagagaaatgagcactgcaaaatga 2983
|||||
Sbjct: 151670 aggtttactggttcaaagatgggaagcagatttctaagagaaatgagcactgcaaaatga 151611

Query: 2984 ggcgagaaggagatgggacatgctctctgcacattgaatccactaccagtgatgacgatg 3043
|||||
Sbjct: 151610 ggcgagaaggagatgggacatgctctctgcacattgaatccactaccagtgatgacgatg 151551

Query: 3044 gcaactacaccatcatggcagccaacccccagg-ggaga 3081
|||||
Sbjct: 151550 gcaactacaccatcatggcagccaacccccagggtggaga 151512

Score = 272 bits (137), Expect = 1e-69
Identities = 137/137 (100%)
Strand = Plus / Minus

Query: 3657 cagtatgcaccaggacacaacagggatgcctgccttctcattcagccagccaagaaatc 3716
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Sbjct: 139264 cagtatgcaccaggacacaacagggatgcctgccttctcattcagccagccaagaaatc 139205

Query: 3717 agacgctggatggtacacgttgtcagccaagaatgaagccggcatcgtgtcgtgcactgc 3776
|||||
Sbjct: 139204 agacgctggatggtacacgttgtcagccaagaatgaagccggcatcgtgtcgtgcactgc 139145

Query: 3777 caggctggatatatacg 3793
|||||
Sbjct: 139144 caggctggatatatacg 139128

Score = 260 bits (131), Expect = 5e-66
Identities = 131/131 (100%)
Strand = Plus / Minus

Query: 3157 aggggaagatcccgagtgcagaaagagacaaagagcccctacaggaacgctttttccga 3216
|||||
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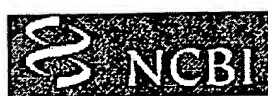
Query: 3217 ccacatttcctgcaggctcctggggataggttagctcatgaggggagcctctgtcggctg 3276
|||||
Sbjct: 148621 ccacatttcctgcaggctcctggggataggttagctcatgaggggagcctctgtcggctg 148562

Query: 3277 gactgtaaggt 3287
|||||
Sbjct: 148561 gactgtaaggt 148551

Score = 173 bits (87), Expect = 1e-39
Identities = 87/87 (100%)
Strand = Plus / Minus

Query: 3073 caggggagaatcagctgttctggccacttgatgggtacaaagtttgccattcgcagtcgg 3132
|||||
Sbjct: 150584 caggggagaatcagctgttctggccacttgatgggtacaaagtttgccattcgcagtcgg 150525

Query: 3133 ctaacctctgctggtcagtctcacagg 3159
|||||||
Sbjct: 150524 ctaacctctgctggtcagtctcacagg 150498



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[Protein](#)
[Genome](#)
[Structure](#)
[PMC](#)
[Taxonomy](#)
[OMIM](#)
[Boo](#)

Search for

Show:

☐ 1: AC024258. Homo sapiens chro...[gi:20564414]

[Links](#)

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 DEFINITION Homo sapiens chromosome 10 clone RP11-297N15, complete sequence.
 ACCESSION AC024258
 VERSION AC024258.9 GI:20564414
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 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 160658)
 AUTHORS Smith,D.R.
 TITLE Genome Therapeutics Corporation Sequencing Center: Human Genome
 Sequence Data
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 160658)
 AUTHORS Smith,D.R.
 TITLE Direct Submission
 JOURNAL Submitted (28-FEB-2000) Genome Therapeutics Corporation, 100 Beaver
 Street, Waltham, MA 02453, USA
 REFERENCE 3 (bases 1 to 160658)
 AUTHORS Smith,D.R.
 TITLE Direct Submission
 JOURNAL Submitted (13-NOV-2001) Genome Therapeutics Corporation, 100 Beaver
 Street, Waltham, MA 02453, USA
 REFERENCE 4 (bases 1 to 160658)
 AUTHORS Smith,D.R.
 TITLE Direct Submission
 JOURNAL Submitted (14-MAY-2002) Genome Therapeutics Corporation, 100 Beaver
 Street, Waltham, MA 02453, USA
 COMMENT On May 14, 2002 this sequence version replaced gi:16905139.
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Nucleotide
 Protein
 Genome
 Structure
 PMC
 Taxonomy
 OMIM
 Boo

Search for
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 Display Show: Send to Get Subsequence Fe

☐ 1: AL512429. Human DNA sequenc...[gi:16508239]

Links

LOCUS AL512429 11170 bp DNA linear PRI 26-OCT-2001
 DEFINITION Human DNA sequence from clone RP11-429C3 on chromosome 10, complete
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 ACCESSION AL512429
 VERSION AL512429.14 GI:16508239
 KEYWORDS HTG.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 11170)

Mashreghi-Mohammadi, M.

Direct Submission

Submitted (26-OCT-2001) Sanger Centre, Hinxton, Cambridgeshire,
 CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
 requests: clonerequest@sanger.ac.uk

COMMENT On Oct 29, 2001 this sequence version replaced gi:15028699.
 During sequence assembly data is compared from overlapping clones.
 Where differences are found these are annotated as variations
 together with a note of the overlapping clone name. Note that the
 variation annotation may not be found in the sequence submission
 corresponding to the overlapping clone, as we submit sequences with
 only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all
 regions were either double-stranded or sequenced with an alternate
 chemistry or covered by high quality data (i.e., phred quality >= 30);
 an attempt was made to resolve all sequencing problems, such
 as compressions and repeats; all regions were covered by at least
 one plasmid subclone or more than one M13 subclone; and the
 assembly was confirmed by restriction digest. The following
 abbreviations are used to associate primary accession numbers given
 in the feature table with their source databases: Em:, EMBL; Sw:,
 SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP
 database can be found at

http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence
 was generated from part of bacterial clone contigs of human
 chromosome 10, constructed by the Sanger Centre Chromosome 10
 Mapping Group. Further information can be found at
<http://www.sanger.ac.uk/HGP/Chr10>


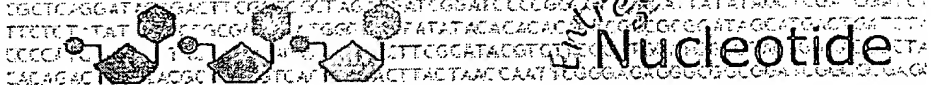
RP11-429C3 is from the library RPCI-11.2 constructed by the group
 of Pieter de Jong. For further details see

<http://www.chori.org/bacpac/home.htm>

VECTOR: pBACe3.6

IMPORTANT: This sequence is not the entire insert of clone
 RP11-429C3 It may be shorter because we sequence overlapping
 sections only once, except for a short overlap.

The true left end of clone RP11-153K11 is at 9171 in this sequence.

  **Nucleotide**

PubMed Nucleotide Protein Genome Structure PMC Taxonomy OMIM Bio

Search for

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Display Show:

☐ 1: AC016395. Homo sapiens chro...[gi:20564406]

Links

LOCUS AC016395 166869 bp DNA linear PRI 14-MAY-2002
DEFINITION Homo sapiens chromosome 10 clone RP11-153K11, complete sequence.
ACCESSION AC016395
VERSION AC016395.5 GI:20564406
KEYWORDS HTG.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 166869)
AUTHORS Smith,D.R.
TITLE Genome Therapeutics Corporation Sequencing Center: Human Genome
Sequence Data
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 166869)
AUTHORS Smith,D.R.
TITLE Direct Submission
JOURNAL Submitted (26-NOV-1999) Genome Therapeutics Corporation, 100 Beaver
Street, Waltham, MA 02453, USA
REFERENCE 3 (bases 1 to 166869)
AUTHORS Smith,D.R.
TITLE Direct Submission
JOURNAL Submitted (26-AUG-2000) Genome Therapeutics Corporation, 100 Beaver
Street, Waltham, MA 02453, USA
REFERENCE 4 (bases 1 to 166869)
AUTHORS Smith,D.R.
TITLE Direct Submission
JOURNAL Submitted (14-MAY-2002) Genome Therapeutics Corporation, 100 Beaver
Street, Waltham, MA 02453, USA
COMMENT On May 14, 2002 this sequence version replaced gi:9929646.
FEATURES
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Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="10"
/clone="RP11-153K11"
/clone_lib="RPCI-11"
BASE COUNT 47408 a 35216 c 35336 g 48909 t
ORIGIN

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121 accactgtag aaattgtggg gaaattttct gtaatgcctg ctctgacaac gaactacctt
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241 gatgctcatc taacttgccc tgagactcca gaactaaatc cttatgtatg aaattaccta
301 caatgaatgt tatgatgttg tatacaaagg taaccagaca gctctcctta agcggctttc
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